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OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/854,208

DATE: 12/04/2001

TIME: 20:15:43

Input Set : N:\Crf3\RULE60\09854208.raw

Output Set: N:\CRF3\12042001\I854208.raw

ENTERED

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1 <110> APPLICANT: Chen, Jian
2   Filvaroff, Ellen
3   Goddard, Audrey
4   Gurney, Austin
5   Li, Hanzhong
6   Wood, William I.
7 <120> TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES
8   THEREOF
9 <130> FILE REFERENCE: P1381-R1
10 <140> CURRENT APPLICATION NUMBER: 09/854,208
11 <141> CURRENT FILING DATE: 2001-05-10
12 <150> PRIOR APPLICATION NUMBER: US/09/311,832
13 <151> PRIOR FILING DATE: 1999-05-14
14 <150> PRIOR APPLICATION NUMBER: US 60/085,579
15 <151> PRIOR FILING DATE: 1998-05-15
16 <150> PRIOR APPLICATION NUMBER: US 60/113,621
17 <151> PRIOR FILING DATE: 1998-12-23
18 <160> NUMBER OF SEQ ID NOS: 26
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 180
22 <212> TYPE: PRT
23 <213> ORGANISM: Homo sapiens
24 <400> SEQUENCE: 1
25   Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile
26       1           5           10           15
27   Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys
28           20           25           30
29   Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val
30           35           40           45
31   Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu
32           50           55           60
33   Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn
34           65           70           75
35   Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu
36           80           85           90
37   Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile
38           95          100          105
39   Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg
40          110          115          120
41   Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp
42          125          130          135
43   Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg
44          140          145          150
45   Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln
46          155          160          165
47   Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
48          170          175          180

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50 <210> SEQ ID NO: 2
51 <211> LENGTH: 687
52 <212> TYPE: DNA
53 <213> ORGANISM: Homo sapiens
54 <400> SEQUENCE: 2
55   aggcgggcag cagctgcagg ctgaccttgc agcttggcgg aatggactgg 50
56   cctcacaacc tgctgtttct tcttaccatt tccatcttcc tggggctggg 100
57   ccagcccagg agccccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150
58   ccctggcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200
59   aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250
60   ggcccagctg aggaacagct cagagctggc ccagagaaaag tgtgagggtca 300
61   acttgcagct gtggatgtcc aacaagagga gcctgtctcc ctggggctac 350
62   agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400
63   gtgcctgtgt ctgggctgtg tgaacccctt caccatgcag gaggaccgca 450
64   gcatggtgag cgtgcccgtg ttcagccagg ttctgtgctg ccgccgcctc 500
65   tgcccgcac cgccccgcac agggccttgc cgccagcgcg cagtcattga 550
66   gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600
67   gccaggccag cagcccagaga ccatactcct tgcacctttg tgccaagaaa 650
68   ggcctatgaa aagtaaacac tgacttttga aagcaag 687
70 <210> SEQ ID NO: 3
71 <211> LENGTH: 197
72 <212> TYPE: PRT
73 <213> ORGANISM: Homo sapiens
74 <400> SEQUENCE: 3
75   Met Thr Leu Leu Pro Gly Leu Leu Phe Leu Thr Trp Leu His Thr
76       1             5             10             15
77   Cys Leu Ala His His Asp Pro Ser Leu Arg Gly His Pro His Ser
78               20             25             30
79   His Gly Thr Pro His Cys Tyr Ser Ala Glu Glu Leu Pro Leu Gly
80               35             40             45
81   Gln Ala Pro Pro His Leu Leu Ala Arg Gly Ala Lys Trp Gly Gln
82               50             55             60
83   Ala Leu Pro Val Ala Leu Val Ser Ser Leu Glu Ala Ala Ser His
84               65             70             75
85   Arg Gly Arg His Glu Arg Pro Ser Ala Thr Thr Gln Cys Pro Val
86               80             85             90
87   Leu Arg Pro Glu Glu Val Leu Glu Ala Asp Thr His Gln Arg Ser
88               95            100            105
89   Ile Ser Pro Trp Arg Tyr Arg Val Asp Thr Asp Glu Asp Arg Tyr
90            110            115            120
91   Pro Gln Lys Leu Ala Phe Ala Glu Cys Leu Cys Arg Gly Cys Ile
92            125            130            135
93   Asp Ala Arg Thr Gly Arg Glu Thr Ala Ala Leu Asn Ser Val Arg
94            140            145            150
95   Leu Leu Gln Ser Leu Leu Val Leu Arg Arg Arg Pro Cys Ser Arg
96            155            160            165
97   Asp Gly Ser Gly Leu Pro Thr Pro Gly Ala Phe Ala Phe His Thr
98            170            175            180
99   Glu Phe Ile His Val Pro Val Gly Cys Thr Cys Val Leu Pro Arg

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100                               185                               190                               195
101      Ser Val
102      197
104 <210> SEQ ID NO: 4
105 <211> LENGTH: 1047
106 <212> TYPE: DNA
107 <213> ORGANISM: Homo sapiens
108 <400> SEQUENCE: 4
109      gccagggtgtg caggccgctc caagcccagc ctgccccgct gccgccacca 50
110      tgacgctcct ccccggcctc ctgtttctga cctggctgca cacatgcctg 100
111      gccaccatg acccctccct cagggggcac cccacagtc acggtacccc 150
112      aactgctac tcggtgagg aactgcccct cggccaggcc cccccacacc 200
113      tgctggctcg aggtgccaag tgggggcagg ctttgctgt agccctggtg 250
114      tccagcctgg aggcagcaag ccacaggggg aggcacgaga ggccctcagc 300
115      tacgaccag tgcccgggtg tcgggcccga ggagggtgtg gaggcagaca 350
116      cccaccagcg ctccatctca ccctggagat accgtgtgga caccgatgag 400
117      gaccgctatc cacagaagct ggccttcgcc gagtgcctgt gcagaggctg 450
118      tatcgatgca cggacggggc gcgagacagc tgcgctcaac tccgtgcggc 500
119      tgctccagag cctgctgggtg ctgcgccgcc ggccctgctc ccgcgacggc 550
120      tcggggctcc ccacacctg ggcccttgcc ttccacaccg agttcatcca 600
121      cgtcccogtc ggctgcacct gcgtgctgcc ccgttcagt tgaccgccga 650
122      ggccgtgggg cccctagact ggacacgtgt gctcccaga gggcaccccc 700
123      tatttatgtg tatttattgt tatttatatg cctcccccaa cactaccctt 750
124      ggggtctggg cattccccgt gtctggagga cagcccccca ctgttctct 800
125      catctccagc ctcagtagtt gggggtagaa ggagctcagc acctcttcca 850
126      gcccttaaag ctgcagaaaa ggtgtcacac ggctgcctgt accttggtc 900
127      cctgtcctgc tcccggcttc ccttacccta tcaactggcct caggccccgc 950
128      aggtgcctc ttcccaacct ccttggaaat acccctgttt cttaaacaat 1000
129      tattaagtg tacgtgtatt attaaactga tgaacacatc cccaaaaa 1047
131 <210> SEQ ID NO: 5
132 <211> LENGTH: 830
133 <212> TYPE: DNA
134 <213> ORGANISM: Homo sapiens
135 <220> FEATURE:
W--> 136 <221> NAME/KEY: unknown
137 <222> LOCATION: 105-115
138 <223> OTHER INFORMATION: unknown base
139 <400> SEQUENCE: 5
140      ggcagcaggg accaagagag gcacgcttgc ccttttatga catcagagct 50
141      cctggttctt gctccttggt actctgggac ttacaccagt ggcaccctg 100
W--> 142      gctcnnnnnn nnnnnaattc ggtacgaggc tggggttcag gcgggcagca 150
143      gctgcaggct gaccttgcag cttggcgga tggactggcc tcacaacctg 200
144      ctgtttcttc ttaccatttc catcttcctg gggctgggcc agcccaggag 250
145      ccccaaaagc aagaggaagg ggcaaggggc gcctggggcc ctggtccctg 300
146      gccctcacca ggtgccactg gacctgggtg cacggatgaa accgtatgcc 350
147      cgcatggagg agtatgagag gaacatcgag gagatgttgg ccagctgag 400
148      gaacagttca gagctggccc agagaaagt tgaggtaaac ttgcagctgt 450
149      ggatgtccaa caagaggagc ctgtctccct ggggctacag catcaaccac 500
150      gacccagcc gtatccccgt ggacctccg aggcacggtg cctgtgtctg 550

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151      ggcttgtgtg aaccccttca ccatgcagga ggaccgcagc atggtgagcg 600
152      tgccggtgtt cagccagggt cctgtgcgcc gccgcctctg cccgccaccg 650
153      ccccgcacag ggccttgccg ccagcgcgca gtcattggaga ccatcgctgt 700
154      gggctgcacc tgcattctct gaatcgacct ggcccagaag ccaggccagc 750
155      agcccagagc catcctcctt gcacctttgt gccaaagaaag gcctatgaaa 800
156      agtaaact gacttttgaa agcaaaaaaa 830
158 <210> SEQ ID NO: 6
159 <211> LENGTH: 397
160 <212> TYPE: DNA
161 <213> ORGANISM: Homo sapiens
162 <220> FEATURE:
W--> 163 <221> NAME/KEY: unknown
164 <222> LOCATION: 10, 150, 267
165 <223> OTHER INFORMATION: unknown base
166 <400> SEQUENCE: 6
W--> 167      aggcgggcan agctgcaggc tgaccttgca gcttggcgga atggactggc 50
168      ctcaaacct gctgtttctt cttaccattt ccatcttctt ggggctgggc 100
W--> 169      agccaggagc cccaaaagca agagggaagg gcaaggcgcg cctggggcccn 150
170      tggcctggcc tcaccagggt cactggacc tgggtgtcac gatgaaaccg 200
171      tatgcccgca tggaggagta tgagaggaa acatcgaggaga tgggtggcca 250
W--> 172      gctgaggaac agctcanaag ctggcccaga gaaagtgtga ggtcaacttg 300
173      cagctgtgga tgtccaacaa gaaggagcct gtctcccttg gggctacaag 350
174      catcaaccac cgaccccagc cgtatccccg tgggaccttg ccgggac 397
176 <210> SEQ ID NO: 7
177 <211> LENGTH: 230
178 <212> TYPE: DNA
179 <213> ORGANISM: Homo sapiens
180 <400> SEQUENCE: 7
181      cacggatgag gaccgctatc cacagaagct ggccttcgcc gaggctctgt 50
182      gcagaggctg tatcgatgca cggacgggcc gcgagacagc tgcgctcaac 100
183      tccgtgcggc tgctccagag cctgctgggt ctgcgcgccg ggccctgtct 150
184      ccgcgacggc tcggggctcc ccacacctgg ggcctttgcc ttccacaccg 200
185      agttcatcca cgtccccgtc ggctgcacct 230
187 <210> SEQ ID NO: 8
188 <211> LENGTH: 24
189 <212> TYPE: DNA
190 <213> ORGANISM: Artificial sequence
191 <220> FEATURE:
W--> 192 <221> NAME/KEY: Artificial Sequence
193 <222> LOCATION: 1-24
194 <223> OTHER INFORMATION: Forward PCR primer
195 <400> SEQUENCE: 8
196      atccacagaa gctggccttc gccg 24
198 <210> SEQ ID NO: 9
199 <211> LENGTH: 24
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial sequence
202 <220> FEATURE:
W--> 203 <221> NAME/KEY: Artificial Sequence

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Input Set : N:\Crf3\RULE60\09854208.raw

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204 <222> LOCATION: 1-24
 205 <223> OTHER INFORMATION: reverse PCR primer
 206 <400> SEQUENCE: 9
 207 gggacgtgga tgaactcggg gtgg 24
 209 <210> SEQ ID NO: 10
 210 <211> LENGTH: 40
 211 <212> TYPE: DNA
 212 <213> ORGANISM: Artificial sequence
 213 <220> FEATURE:
 W--> 214 <221> NAME/KEY: Artificial Sequence
 215 <222> LOCATION: 1-40
 216 <223> OTHER INFORMATION: hybridization probe
 217 <400> SEQUENCE: 10
 218 tatccacaga agctggcctt cgccgagtgct ctgtgcagag 40
 220 <210> SEQ ID NO: 11
 221 <211> LENGTH: 155
 222 <212> TYPE: PRT
 223 <213> ORGANISM: Homo sapiens
 224 <400> SEQUENCE: 11
 225 Met Thr Pro Gly Lys Thr Ser Leu Val Ser Leu Leu Leu Leu Leu
 226 1 5 10 15
 227 Ser Leu Glu Ala Ile Val Lys Ala Gly Ile Thr Ile Pro Arg Asn
 228 20 25 30
 229 Pro Gly Cys Pro Asn Ser Glu Asp Lys Asn Phe Pro Arg Thr Val
 230 35 40 45
 231 Met Val Asn Leu Asn Ile His Asn Arg Asn Thr Asn Thr Asn Pro
 232 50 55 60
 233 Lys Arg Ser Ser Asp Tyr Tyr Asn Arg Ser Thr Ser Pro Trp Asn
 234 65 70 75
 235 Leu His Arg Asn Glu Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp
 236 80 85 90
 237 Glu Ala Lys Cys Arg His Leu Gly Cys Ile Asn Ala Asp Gly Asn
 238 95 100 105
 239 Val Asp Tyr His Met Asn Ser Val Pro Ile Gln Gln Glu Ile Leu
 240 110 115 120
 241 Val Leu Arg Arg Glu Pro Pro His Cys Pro Asn Ser Phe Arg Leu
 242 125 130 135
 243 Glu Lys Ile Leu Val Ser Val Gly Cys Thr Cys Val Thr Pro Ile
 244 140 145 150
 245 Val His His Val Ala
 246 155
 248 <210> SEQ ID NO: 12
 249 <211> LENGTH: 408
 250 <212> TYPE: PRT
 C--> 251 <213> ORGANISM: Artificial
 252 <220> FEATURE:
 W--> 253 <221> NAME/KEY: Artificial Sequence
 254 <222> LOCATION: 1-408
 255 <223> OTHER INFORMATION: IL17B-Fc fusion

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/854,208

DATE: 12/04/2001

TIME: 20:15:44

Input Set : N:\Crf3\RULE60\09854208.raw

Output Set: N:\CRF3\12042001\I854208.raw

L:136 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:142 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:163 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:192 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:203 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:214 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:251 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:253 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:317 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:319 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:506 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:508 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
L:546 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:548 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:557 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:559 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
L:619 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:621 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
L:653 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:655 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:24